

# SEQUENCE LISTING

<110> Chapman, Edwin R.  
Dong, Min

<120> BOTULINUM NEUROTOXIN B RECEPTORS AND USE THEREOF

<130> 960296.99004

<150> 60/422,951

<151> 2002-10-31

<150> 60/498,128

<151> 2003-08-27

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<170> PatentIn version 3.2

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Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly  
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<211> 422  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE

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<222> (33)..(53)
<223> BoNT/B binding domain

<220>
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<222> (54)..(80)
<223> Gangliosides binding domain or transmembrane domain

<400> 5

Met Val Ser Glu Ser His His Glu Ala Leu Ala Ala Pro Pro Val Thr
1          5          10          15

Thr Val Ala Thr Val Leu Pro Ser Asn Ala Thr Glu Pro Ala Ser Pro
20          25          30

Gly Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Glu Lys Phe Met
35          40          45

Asn Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile
50          55          60

Ala Ile Val Ala Val Leu Leu Val Leu Thr Cys Cys Phe Cys Ile Cys
65          70          75          80

Lys Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys
85          90          95

Gly Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys
100         105         110

Thr Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu
115         120         125

Thr Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly
130         135         140

Lys Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu
145         150         155         160

Val Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly
165         170         175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys
180         185         190

Lys Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn
195         200         205

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Glu Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr  
210 215 220

Leu Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile  
225 230 235 240

Ile Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val  
245 250 255

Thr Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu  
260 265 270

Lys Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly  
275 280 285

Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp  
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn  
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu  
325 330 335

Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln  
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile  
355 360 365

Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr  
370 375 380

Gly Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg  
385 390 395 400

Pro Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala  
405 410 415

Met Leu Ala Val Lys Lys  
420

<210> 6  
<211> 1876  
<212> DNA  
<213> Mus musculus

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<220>
<221> CDS
<222> (16)..(1284)

<220>
<221> misc_feature
<222> (133)..(195)
<223> BoNT/B binding domain

<220>
<221> misc_feature
<222> (196)..(276)
<223> Gangliosides binding domain or transmembrane domain

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      Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Asn
              1              5              10

gtg gct ccg gcc acc acc act gcc aca atg ccc ctt gca ccc gtc gca      99
Val Ala Pro Ala Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Val Ala
      15              20              25

cct gcc gac aac tct aca gag agc acg ggt cct ggg gag agc caa gaa      147
Pro Ala Asp Asn Ser Thr Glu Ser Thr Gly Pro Gly Glu Ser Gln Glu
      30              35              40

gac atg ttc gcc aag ctg aag gag aaa ttc ttc aat gag atc aac aag      195
Asp Met Phe Ala Lys Leu Lys Glu Lys Phe Phe Asn Glu Ile Asn Lys
      45              50              55              60

atc ccc ttg ccc ccc tgg gct ctg atc gcc atg gct gtg gtt gct ggc      243
Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly
              65              70              75

ctc ctg ctg ctc acc tgt tgc ttc tgc atc tgt aag aag tgc tgc tgc      291
Leu Leu Leu Leu Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys
      80              85              90

aag aag aag aag aac aag aag gag aag ggc aaa ggc atg aag aac gcc      339
Lys Lys Lys Lys Asn Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala
      95              100              105

atg aac atg aag gac atg aaa ggc ggc cag gat gac gat gat gca gag      387
Met Asn Met Lys Asp Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu
      110              115              120

aca ggc ctg act gaa gga gaa ggt gaa ggc gag gag gag aaa gag cca      435
Thr Gly Leu Thr Glu Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro
      125              130              135              140

gag aac ctg ggc aaa ttg cag ttt tct ctg gac tat gat ttc cag gcc      483
Glu Asn Leu Gly Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala
      145              150              155

aac cag ctc acc gtg ggt gtc ctg cag gct gcg gaa ctc cca gcc ctg      531
Asn Gln Leu Thr Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu
      160              165              170

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gac atg ggt ggc aca tca gac cct tat gtc aaa gtc ttc ctc ctc cca	579
Asp Met Gly Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro	
175 180 185	
gac aag aag aag aaa tat gag act aag gtg cat cgg aag acg ctg aac	627
Asp Lys Lys Lys Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn	
190 195 200	
cca gcc ttc aat gag aca ttc act ttc aag gtg cca tac cag gag tta	675
Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu	
205 210 215 220	
gca ggc aag acc ctg gtg atg gca atc tat gac ttt gac cgc ttc tct	723
Ala Gly Lys Thr Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser	
225 230 235	
aag cat gac atc atc ggg gag gtg aag gta ccc atg aac aca gtg gac	771
Lys His Asp Ile Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp	
240 245 250	
ctt ggc cag ccc atc gag gaa tgg aga gac cta caa ggc gga gag aag	819
Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys	
255 260 265	
gaa gag cca gag aag ttg ggt gac atc tgt acc tcc ttg cgc tac gtg	867
Glu Glu Pro Glu Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val	
270 275 280	
ccc aca gct ggg aag ctc acc gtc tgt atc ctg gag gcc aag aac ctg	915
Pro Thr Ala Gly Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu	
285 290 295 300	
aag aag atg gac gta ggg ggc ctt tca gac ccc tat gtg aag atc cac	963
Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His	
305 310 315	
ctg atg cag aac ggt aag aga ctc aag aag aag aag acg aca gtg aag	1011
Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys	
320 325 330	
aag aag acc ctg aac ccc tac ttc aac gag tcc ttc agc ttc gag atc	1059
Lys Lys Thr Leu Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile	
335 340 345	
ccc ttt gag cag atc cag aaa gtc cag gtg gtc gtc acc gtg cta gac	1107
Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp	
350 355 360	
tac gac aaa ctg ggc aag aat gaa gcc atc gga aag atc ttt gta ggc	1155
Tyr Asp Lys Leu Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly	
365 370 375 380	
agc aac gcc aca ggc acc gag ttg cgg cac tgg tcc gac atg ctg gcc	1203
Ser Asn Ala Thr Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala	
385 390 395	
aac cct cgg agg ccc att gcc cag tgg cac tct ctt aag cct gag gaa	1251
Asn Pro Arg Arg Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu	
400 405 410	
gaa gtg gat gct ctt ctg ggc aag aac aag tag gctccagcgg ccggtgccac	1304

Glu Val Asp Ala Leu Leu Gly Lys Asn Lys  
 415 420

gcccctaagg agccacgccc ccgaggcgcc acgccccctg aggacactga cgagatccag 1364  
 agctatcaat acctcagtta cgcgacctta gaggtttctt catttgtttg cgggtgtgtcc 1424  
 tgtttttcct tcctttttct ctttttaaag accaacttcc ttttggtggc tgtgtgaaga 1484  
 gagtccccta agaggtgaaa gaaaagcctg gctctgttat tgtccccgga gcggtccttg 1544  
 ttgcatgccc tttaacgggtt tcccccttac cccaagtggg gccctctact gtcagacagt 1604  
 tgaagcacta actgcttttc ctgggttttg gaccaacaac atggcaagca cattctgttt 1664  
 cttgactgtg aaggcaacat agtggccagc attgtgtgtg tgtgtgtgtg tgtgtgtgtg 1724  
 tatgtgtgtg tgtacacctg tatgtgccca tccatcccca cctgcctggt ttgaacatct 1784  
 ctcttcattt tctggaatga gtcatggaca gtgaagccat gtgagaggag aatgtcttca 1844  
 gagactccaa gggaaagcaa gccactgcc tg 1876

<210> 7  
 <211> 422  
 <212> PRT  
 <213> Mus musculus

<400> 7

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Asn Val Ala Pro Ala  
 1 5 10 15

Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Val Ala Pro Ala Asp Asn  
 20 25 30

Ser Thr Glu Ser Thr Gly Pro Gly Glu Ser Gln Glu Asp Met Phe Ala  
 35 40 45

Lys Leu Lys Glu Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro  
 50 55 60

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu  
 65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys  
 85 90 95

Asn Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys  
 100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Ala Glu Thr Gly Leu Thr  
 115 120 125



Glu Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly  
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr  
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly  
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys  
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn  
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Ala Gly Lys Thr  
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile  
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro  
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu  
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly  
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp  
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn  
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu  
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln  
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu  
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr  
 370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg  
 385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala  
 405 410 415

Leu Leu Gly Lys Asn Lys  
 420

<210> 8  
 <211> 2681  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <221> CDS  
 <222> (115)..(1383)

<220>  
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 <222> (232)..(294)  
 <223> BoNT/B binding domain

<220>  
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 <222> (295)..(375)  
 <223> Gangliosides binding domain or transmembrane domain

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 ggtccccctct tcccaactccc gcgccggcca gcgctgcggc tccccctctgc cacc atg 117  
 Met  
 1

aga aac atc ttc aag agg aac cag gag ccc att gtg gct ccg gcc acc 165  
 Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala Thr  
 5 10 15

acc act gcc aca atg cct ctg gca ccc gcc gca cct gcc gat aac tct 213  
 Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn Ser  
 20 25 30

aca gag agc acg ggc acc ggg gag agc caa gaa gac atg ttc gcc aag 261  
 Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala Lys  
 35 40 45

ctg aag gac aaa ttc ttc aat gag atc aac aag atc cct ttg ccc ccc 309  
 Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro  
 50 55 60 65

tgg gct ctg att gcc atg gcc gtg gtt gct ggc ctc ctg ctg ctc acc 357

Trp	Ala	Leu	Ile	Ala	Met	Ala	Val	Val	Ala	Gly	Leu	Leu	Leu	Leu	Thr	
			70						75					80		
tgc	tgc	ttc	tgc	atc	tgt	aag	aag	tgc	tgc	tgc	aag	aag	aag	aaa	aac	405
Cys	Cys	Phe	Cys	Ile	Cys	Lys	Lys	Cys	Cys	Cys	Lys	Lys	Lys	Lys	Asn	
			85					90					95			
aag	aag	gag	aag	ggc	aaa	ggc	atg	aag	aac	gcc	atg	aac	atg	aag	gac	453
Lys	Lys	Glu	Lys	Gly	Lys	Gly	Met	Lys	Asn	Ala	Met	Asn	Met	Lys	Asp	
		100					105					110				
atg	aag	ggg	ggc	cag	gat	gat	gac	gac	gag	aca	ggc	ctg	act	gaa		501
Met	Lys	Gly	Gly	Gln	Asp	Asp	Asp	Asp	Ala	Glu	Thr	Gly	Leu	Thr	Glu	
	115					120					125					
gga	gaa	gga	gaa	ggc	gag	gag	gag	aaa	gag	ccg	gag	aac	ctg	ggc	aaa	549
Gly	Glu	Gly	Glu	Gly	Glu	Glu	Glu	Lys	Glu	Pro	Glu	Asn	Leu	Gly	Lys	
130					135				140					145		
ttg	cag	ttt	tct	ctg	gac	tat	gat	ttc	caa	gcc	aac	cag	ctc	acc	gtg	597
Leu	Gln	Phe	Ser	Leu	Asp	Tyr	Asp	Phe	Gln	Ala	Asn	Gln	Leu	Thr	Val	
				150					155					160		
ggc	gtc	ctg	cag	gct	gct	gaa	ctc	ccg	gcc	ctg	gac	atg	ggg	ggc	acg	645
Gly	Val	Leu	Gln	Ala	Ala	Glu	Leu	Pro	Ala	Leu	Asp	Met	Gly	Gly	Thr	
			165					170					175			
tca	gac	cct	tac	gtc	aaa	gtc	ttc	ctc	ctc	cca	gac	aag	aag	aag	aaa	693
Ser	Asp	Pro	Tyr	Val	Lys	Val	Phe	Leu	Leu	Pro	Asp	Lys	Lys	Lys	Lys	
		180					185					190				
tat	gag	acc	aag	gtg	cac	cgg	aag	aca	ctg	aac	cca	gcc	ttc	aac	gaa	741
Tyr	Glu	Thr	Lys	Val	His	Arg	Lys	Thr	Leu	Asn	Pro	Ala	Phe	Asn	Glu	
	195					200					205					
act	ttc	act	ttc	aag	gtg	cca	tac	cag	gag	tta	gga	ggc	aaa	acc	ctg	789
Thr	Phe	Thr	Phe	Lys	Val	Pro	Tyr	Gln	Glu	Leu	Gly	Gly	Lys	Thr	Leu	
210					215				220					225		
gtg	atg	gct	atc	tat	gac	ttt	gac	cgc	ttc	tct	aag	cat	gac	atc	atc	837
Val	Met	Ala	Ile	Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile	
			230					235						240		
ggg	gag	gtg	aaa	gtg	ccc	atg	aac	acg	gtg	gac	ctt	ggc	cag	ccc	atc	885
Gly	Glu	Val	Lys	Val	Pro	Met	Asn	Thr	Val	Asp	Leu	Gly	Gln	Pro	Ile	
			245					250					255			
gag	gaa	tgg	aga	gac	cta	caa	ggc	gga	gag	aag	gaa	gag	cca	gag	aag	933
Glu	Glu	Trp	Arg	Asp	Leu	Gln	Gly	Gly	Glu	Lys	Glu	Glu	Pro	Glu	Lys	
		260					265					270				
ctg	ggg	gac	atc	tgt	acc	tcc	ttg	cgc	tac	gtg	ccc	act	gct	ggg	aag	981
Leu	Gly	Asp	Ile	Cys	Thr	Ser	Leu	Arg	Tyr	Val	Pro	Thr	Ala	Gly	Lys	
	275					280					285					
ctc	acc	gtc	tgt	atc	ctg	gag	gcc	aag	aac	ctg	aag	aag	atg	gat	gtg	1029
Leu	Thr	Val	Cys	Ile	Leu	Glu	Ala	Lys	Asn	Leu	Lys	Lys	Met	Asp	Val	
290					295				300					305		
ggg	ggc	ctc	tca	gac	ccc	tat	gtg	aag	atc	cac	ttg	atg	cag	aat	ggc	1077
Gly	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Ile	His	Leu	Met	Gln	Asn	Gly	

310	315	320	
aag aga ctc aag aag aag aag acg acg gtg aag aag aag acc ttg aac			1125
Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu Asn			
325	330	335	
ccc tac ttc aat gag tca ttc agc ttc gag atc ccc ttt gag cag atc			1173
Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile			
340	345	350	
cag aaa gtc cag gtg gtc gtc acc gtg cta gac tat gac aaa ctg ggc			1221
Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly			
355	360	365	
aag aat gaa gcc atc gga aag atc ttc gta ggc agc aac gct aca ggc			1269
Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly			
370	375	380	385
acg gag ctg cgg cac tgg tcc gac atg ctg gcg aac cct cgg agg ccc			1317
Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro			
390	395	400	
atc gcc cag tgg cac tct ctg aag cct gag gaa gaa gtg gat gct ctt			1365
Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala Leu			
405	410	415	
ctg ggc aag aac aag tag gcagcggcgc ctggggccac gccccagagg			1413
Leu Gly Lys Asn Lys			
420			
acactgacga gctccagagc tatcaataacc tcagttatgc gaccttagag gtttcttcat			1473
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cttccttttg gtggctatgt gaagaggccc ctaagacgtg aaagagaagc ctggctctgt			1593
tattgtccca ggagctgtcc ttgttgcatg ccctatcacg gttgcccctc accccaagtg			1653
gggccctcta ctgtcagagt ggaagcactt cctgcttttc ctgggttttg gaccaacaaa			1713
gtggcaagca cattctgtgt ctgactgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg			1773
tgtgtgtgtg tgtgtgtgta cacgtgtgcc catccatccc caccttgccct ctgtttggaa			1833
tatctcttcg tttctggaat ggtcacgga caatgatgcc gtgtgagaga ggaaagtctt			1893
caggtactcc gaggtgagga gagccactg ctttaagtggc cagaggccag aagctctcat			1953
agtccttgcg aaaggccatt tggaagacgc aagatgtgat actggatgta ttccgaacta			2013
ggaccaaagg cttgatgcca tcccagactc cctcttgctc gtcattggctt cccaggagt			2073
ggggcttttg gatcattcat gaaaataaac tatttactcg actggtcgga ttcagccagg			2133
gaccgccagc tccaggatgt cattcttggt gacgacatca aactttgaag aaacagaagt			2193
cccattactc agctctggat ctttgccctg tccagtggga ggcagatgct tcctccctct			2253
gcagagtaca agcagtgcgt tcatttgcat tcacgcacca tctgcttttg cctctgtttc			2313
cctttttgtg taagtggaaa aataccatct gacgataagt gctttgcaca gagccagaga			2373

cctattagag ggatgcttgg gtgttttagtt cccttgaggt ccaggtaagg aggaggtgtc 2433  
aagaagggga gcgttggtgg acagtgacaa gctagacatt gcagagctcc tcacaactcc 2493  
tattcctgac cctctggacc ctttgaccct cagtgatggg agccggagta gcccaggcag 2553  
accttaggag aggccccgtc cttcccttcc ttagacagtt ttctcagaat gccaggaaac 2613  
acagcgcatt catttcagat ggggtggtgga gaaaatgtgc taaggtttgc accctatgtt 2673  
cggaattc 2681

<210> 9  
<211> 422  
<212> PRT  
<213> Rattus norvegicus

<400> 9

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala  
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn  
20 25 30

Ser Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala  
35 40 45

Lys Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro  
50 55 60

Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu  
65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys  
85 90 95

Asn Lys Lys Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys  
100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr  
115 120 125

Glu Gly Glu Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly  
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr  
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly  
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys  
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn  
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr  
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile  
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro  
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu  
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly  
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp  
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn  
305 310 315 320

Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu  
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln  
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu  
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr  
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg  
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala

405

410

415

Leu Leu Gly Lys Asn Lys  
420

<210> 10  
<211> 419  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (37)..(57)  
<223> BoNT/B binding domain

<220>  
<221> MISC\_FEATURE  
<222> (58)..(84)  
<223> Gangliosides binding domain or transmembrane domain

<400> 10

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala  
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Ile Gly Pro Val Asp Asn Ser Thr Glu  
20 25 30

Ser Gly Gly Ala Gly Glu Ser Gln Glu Asp Met Phe Ala Lys Leu Lys  
35 40 45

Glu Lys Leu Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro Trp Ala  
50 55 60

Leu Ile Ala Ile Ala Val Val Ala Gly Leu Leu Leu Leu Thr Cys Cys  
65 70 75 80

Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys Asn Lys Lys  
85 90 95

Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp Met Lys  
100 105 110

Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu Gly Glu  
115 120 125

Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys Leu Gln  
130 135 140

Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val  
145 150 155 160

Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp  
165 170 175

Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu  
180 185 190

Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe  
195 200 205

Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met  
210 215 220

Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu  
225 230 235 240

Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu  
245 250 255

Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu Lys Leu Gly  
260 265 270

Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr  
275 280 285

Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly  
290 295 300

Leu Ser Asp Pro Tyr Gly Lys Ile His Leu Met Gln Asn Gly Lys Arg  
305 310 315 320

Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu Asn Pro Tyr  
325 330 335

Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile Gln Lys  
340 345 350

Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly Lys Asn  
355 360 365

Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly Thr Glu  
370 375 380

Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala



385

390

395

400

Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala Leu Leu Gly  
405 410 415

Lys Asn Lys